



#5

SEQUENCE LISTING

<110> FEDER, J.N.

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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY4,
EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG

<130> D0039NP

<140> 09/966,459

<141> 2001-09-26

<150> 60/235,833

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<170> PatentIn Ver. 2.1

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Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
 35 40 45

Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
 50 55 60

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
 65 70 75 80

Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
 85 90 95

Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
 100 105 110

Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125

Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
 130 135 140

Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
 145 150 155 160

Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
 165 170 175

Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
 180 185 190

Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
 195 200 205

Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
 210 215 220

Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
 225 230 235 240

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
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Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
 260 265 270

Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
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Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
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<212> DNA

<213> Homo sapiens

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<213> Artificial Sequence

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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
oligos

<400> 6

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<210> 7

<211> 25

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
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<211> 311
<212> PRT
<213> MOUSE

<400> 8

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Tyr Phe Ser Ile Ile Val Gly Asn Gly Thr Leu Leu Phe Ile Ile Trp
35 40 45

Ser Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Val Leu
50 55 60

Ala Ser Met Asp Leu Gly Met Thr Leu Thr Thr Met Pro Thr Val Leu
65 70 75 80

Gly Val Leu Val Leu Asn Gln Arg Glu Ile Val His Gly Ala Cys Phe
85 90 95

Ile Gln Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val
100 105 110

Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu
115 120 125

His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu
130 135 140

Gly Ala Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro
145 150 155 160

Leu Phe Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe
165 170 175

Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe
180 185 190

Asn Leu Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp
195 200 205

Ala Leu Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met
210 215 220

Gly Ile Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val

225 230 235 240
 Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu
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 Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile
 260 265 270
 Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile
 275 280 285
 Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu
 290 295 300
 Leu Ser Lys His Ser Arg Thr
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 <210> 9
 <211> 307
 <212> PRT
 <213> MOUSE

 <400> 9
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 20 25 30
 Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile Lys
 35 40 45
 Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
 50 55 60
 Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val Met
 65 70 75 80
 Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys Phe
 85 90 95
 Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly Val
 100 105 110
 Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu
 115 120 125

His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Ile Ala Ile Gly Leu
 130 135 140

Gly Val Val Leu Arg Gly Phe Leu Ser Leu Val Pro Pro Ile Leu Pro
 145 150 155 160

Leu Phe Trp Phe Ser Tyr Cys Arg Ser His Val Leu Ser His Ala Phe
 165 170 175

Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe
 180 185 190

Asn Arg Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp
 195 200 205

Ala Leu Ile Ile Val Phe Ser Tyr Val Leu Ile Leu Lys Thr Val Met
 210 215 220

Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Val
 225 230 235 240

Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu
 245 250 255

Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile
 260 265 270

Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile
 275 280 285

Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Val Leu His Leu
 290 295 300

Leu Ser Val
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<210> 10
 <211> 312
 <212> PRT
 <213> HUMAN

<400> 10
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Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val
 20 25 30

Tyr	Val	Cys	Ile	Leu	Leu	Gly	Asn	Gly	Met	Leu	Leu	Tyr	Leu	Ile	Lys	35	40	45	
His	Asp	His	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Phe	Leu	Thr	Met	Leu	50	55	60	
Ala	Gly	Thr	Asp	Leu	Met	Val	Thr	Leu	Thr	Thr	Met	Pro	Thr	Val	Met	65	70	75	80
Gly	Ile	Leu	Trp	Val	Asn	His	Arg	Glu	Ile	Ser	Ser	Val	Gly	Cys	Phe	85	90	95	
Leu	Gln	Ala	Tyr	Phe	Ile	His	Ser	Leu	Ser	Val	Val	Glu	Ser	Gly	Ser	100	105	110	
Leu	Leu	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Ile	Ala	Ile	Arg	Asn	Pro	Leu	115	120	125	
Arg	Tyr	Ala	Ser	Ile	Phe	Thr	Asn	Thr	Arg	Val	Ile	Ala	Leu	Gly	Val	130	135	140	
Gly	Val	Phe	Leu	Arg	Gly	Phe	Val	Ser	Ile	Leu	Pro	Val	Ile	Leu	Arg	145	150	155	160
Leu	Phe	Ser	Phe	Ser	Tyr	Cys	Lys	Ser	His	Val	Ile	Thr	Arg	Ala	Phe	165	170	175	
Cys	Leu	His	Gln	Glu	Ile	Met	Arg	Leu	Ala	Cys	Ala	Asp	Ile	Thr	Phe	180	185	190	
Asn	Arg	Leu	Tyr	Pro	Val	Ile	Leu	Ile	Ser	Leu	Thr	Ile	Phe	Leu	Asp	195	200	205	
Ser	Leu	Ile	Ile	Leu	Phe	Ser	Tyr	Ile	Leu	Ile	Leu	Asn	Thr	Val	Ile	210	215	220	
Gly	Ile	Ala	Ser	Gly	Glu	Glu	Gln	Thr	Lys	Ala	Leu	Asn	Thr	Cys	Val	225	230	235	240
Ser	His	Phe	Cys	Ala	Val	Leu	Ile	Phe	Tyr	Ile	Pro	Leu	Ala	Gly	Leu	245	250	255	
Ser	Ile	Ile	His	Arg	Tyr	Gly	Arg	Asn	Ala	Pro	Pro	Ile	Ser	His	Ala	260	265	270	
Val	Met	Ala	Asn	Val	Tyr	Leu	Phe	Val	Pro	Pro	Ile	Leu	Asn	Pro	Val	275	280	285	

Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
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Leu Ser Lys His Arg Phe Ser Arg
 305 310

<210> 11
 <211> 319
 <212> PRT
 <213> CHICKEN

<400> 11
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Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro Phe Gly
 20 25 30

Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu Leu Val
 35 40 45

Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe Leu Leu
 50 55 60

Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu Pro Thr
 65 70 75 80

Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe Pro Ala
 85 90 95

Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met Glu Ser
 100 105 110

Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125

Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala Gln Ile
 130 135 140

Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro Leu Ile
 145 150 155 160

Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu Ser His
 165 170 175

Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr Asp Ala

180	185	190
Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala Ile Leu		
195	200	205
Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Ile Phe Arg Thr Val		
210	215	220
Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys		
225	230	235 240
Val Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly		
245	250	255
Leu Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His		
260	265	270
Ala Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro		
275	280	285
Val Leu Tyr Ser Met Lys Ser Lys Ala Ile Cys Lys Gly Leu Leu Arg		
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Leu Leu Cys Gln Arg Ala Ala Trp Pro Gly His Ala Gln Asn Cys		
305	310	315

<210> 12
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<400> 12

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Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val		
35	40	45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met		
50	55	60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile		
65	70	75 80

Leu	Ala	Leu	Phe	Trp	Phe	Asp	Ser	Arg	Glu	Ile	Thr	Phe	Asp	Ala	Cys	85	90	95	
Leu	Ala	Gln	Met	Phe	Phe	Ile	His	Ala	Leu	Ser	Ala	Ile	Glu	Ser	Thr	100	105	110	
Ile	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	115	120	125	
Leu	Arg	His	Ala	Ala	Val	Leu	Asn	Asn	Thr	Val	Thr	Val	Gln	Ile	Gly	130	135	140	
Met	Val	Ala	Leu	Val	Arg	Gly	Ser	Leu	Phe	Phe	Phe	Pro	Leu	Pro	Leu	145	150	155	160
Leu	Ile	Lys	Arg	Leu	Ala	Phe	Cys	His	Ser	Asn	Val	Leu	Ser	His	Ser	165	170	175	
Tyr	Cys	Val	His	Gln	Asp	Val	Met	Lys	Leu	Ala	Tyr	Thr	Asp	Thr	Leu	180	185	190	
Pro	Asn	Val	Val	Tyr	Gly	Leu	Thr	Ala	Ile	Leu	Leu	Val	Met	Gly	Val	195	200	205	
Asp	Val	Met	Phe	Ile	Ser	Leu	Ser	Tyr	Phe	Leu	Ile	Ile	Arg	Ala	Val	210	215	220	
Leu	Gln	Leu	Pro	Ser	Lys	Ser	Glu	Arg	Ala	Lys	Ala	Phe	Gly	Thr	Cys	225	230	235	240
Val	Ser	His	Ile	Gly	Val	Val	Leu	Ala	Phe	Tyr	Val	Pro	Leu	Ile	Gly	245	250	255	
Leu	Ser	Val	Val	His	Arg	Phe	Gly	Asn	Ser	Leu	Asp	Pro	Ile	Val	His	260	265	270	
Val	Leu	Met	Gly	Asp	Val	Tyr	Leu	Leu	Leu	Pro	Pro	Val	Ile	Asn	Pro	275	280	285	
Ile	Ile	Tyr	Gly	Ala	Lys	Thr	Lys	Gln	Ile	Arg	Thr	Arg	Val	Leu	Ala	290	295	300	
Met	Phe	Lys	Ile	Ser	Cys	Asp	Lys	Asp	Ile	Glu	Ala	Gly	Gly	Asn	Thr	305	310	315	320

<210> 13
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<212> PRT
<213> MOUSE

<400> 13

Met	Asn	Ser	Lys	Ala	Ser	Met	Leu	Gly	Thr	Asn	Phe	Thr	Ile	Ile	His
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			20					25					30		
Thr	Trp	Leu	Ser	Ile	Pro	Phe	Cys	Leu	Met	Tyr	Ile	Ala	Ala	Val	Leu
		35					40						45		
Gly	Asn	Gly	Ala	Leu	Ile	Leu	Val	Val	Leu	Ser	Glu	Arg	Thr	Leu	His
	50					55					60				
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65					70					75					80
Leu	Ser	Thr	Thr	Thr	Val	Pro	Lys	Thr	Leu	Ala	Ile	Phe	Trp	Phe	His
					85				90					95	
Ala	Gly	Glu	Ile	Pro	Phe	Asp	Ala	Cys	Ile	Ala	Gln	Met	Phe	Phe	Ile
			100					105					110		
His	Val	Ala	Phe	Val	Ala	Glu	Ser	Gly	Ile	Leu	Leu	Ala	Met	Ala	Phe
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Asp	Arg	Tyr	Val	Ala	Ile	Cys	Thr	Pro	Leu	Arg	Tyr	Ser	Ala	Val	Leu
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Thr	Pro	Met	Ala	Ile	Gly	Lys	Met	Thr	Leu	Ala	Ile	Trp	Gly	Arg	Ser
145					150					155					160
Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ile	Phe	Leu	Leu	Lys	Arg	Leu	Ser	Tyr
			165						170					175	
Cys	Arg	Thr	Asn	Val	Ile	Pro	His	Ser	Tyr	Cys	Glu	His	Ile	Gly	Val
		180						185					190		
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Ser	Val	Pro	Met	Ala	Ser	Val	Leu	Val	Asp	Val	Ala	Leu	Ile	Gly	Ile
	210					215					220				

Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe Arg Leu Pro Ser Gln Asp
 225 230 235 240

Ala Arg His Lys Ala Leu Asn Thr Cys Gly Ser His Ile Gly Val Ile
 245 250 255

Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr Phe Leu Thr His Arg Phe
 260 265 270

Gly Lys Asn Ile Pro His His Val His Ile Leu Leu Ala Asn Leu Tyr
 275 280 285

Val Leu Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Ala Lys Thr
 290 295 300

Lys Gln Ile Arg Asp Ser Met Thr Arg Met Leu Ser Val Val Trp Lys
 305 310 315 320

Ser

<210> 14
 <211> 326
 <212> PRT
 <213> MOUSE

<400> 14
 Met Lys Val Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val
 1 5 10 15

Trp Tyr Val Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp
 20 25 30

Ile Ala Ile Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn
 35 40 45

Val Leu Leu Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro
 50 55 60

Met Tyr Phe Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser
 65 70 75 80

Thr Ala Thr Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg
 85 90 95

Gly Ile Ser Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe

100	105	110
Ile Phe Val Ala Glu Ser Ala	Ile Leu Leu Ala Met	Ala Phe Asp Arg
115	120	125
Tyr Val Ala Ile Cys Tyr Pro	Leu Arg Tyr Thr Thr	Ile Leu Thr Ser
130	135	140
Ser Val Ile Gly Lys Ile Gly	Thr Ala Ala Val Val	Arg Ser Phe Leu
145	150	155 160
Ile Cys Phe Pro Phe Ile Phe	Leu Val Tyr Arg Leu Leu	Tyr Cys Gly
165	170	175
Lys His Ile Ile Pro His Ser	Tyr Cys Glu His Met Gly	Ile Ala Arg
180	185	190
Leu Ala Cys Asp Asn Ile Thr	Val Asn Ile Ile Tyr Gly	Leu Thr Met
195	200	205
Ala Leu Leu Ser Thr Gly Leu	Asp Ile Leu Leu Ile Ile	Ile Ser Tyr
210	215	220
Thr Met Ile Leu Arg Thr Val	Phe Gln Ile Pro Ser Trp	Ala Ala Arg
225	230	235 240
Tyr Lys Ala Leu Asn Thr Cys	Gly Ser His Ile Cys Val	Ile Leu Leu
245	250	255
Phe Tyr Thr Pro Ala Phe Phe	Ser Phe Phe Ala His Arg	Phe Gly Gly
260	265	270
Lys Thr Val Pro Arg His Ile	His Ile Leu Val Ala Asn	Leu Tyr Val
275	280	285
Val Val Pro Pro Met Leu Asn	Pro Ile Ile Tyr Gly Val	Lys Thr Lys
290	295	300
Gln Ile Gln Asp Arg Val Val	Phe Leu Phe Ser Ser Val	Ser Thr Cys
305	310	315 320
Gln His Asp Ser Arg Cys		
325		

<210> 15
 <211> 318
 <212> PRT

<213> MOUSE

<220>

<221> MOD_RES

<222> (286)

<223> Xaa represents any amino acid residue.

<400> 15

Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu
1 5 10 15

Leu Gly Ile Pro Gly Leu Glu Glu Leu Gln Phe Trp Leu Gly Leu Pro
20 25 30

Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu
35 40 45

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val
65 70 75 80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe
85 90 95

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile
100 105 110

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
115 120 125

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys
130 135 140

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro
145 150 155 160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile
165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His

210	215	220
Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn		
225	230	235 240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala		
245	250	255
Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr		
260	265	270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu		
275	280	285
Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala		
290	295	300
Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp		
305	310	315

<210> 16
 <211> 316
 <212> PRT
 <213> MOUSE

<400> 16

Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro Ser Val Leu Thr Leu
1 5 10 15
Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro
20 25 30
Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu
35 40 45
Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe
50 55 60
Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu
65 70 75 80
Pro Lys Met Leu Gly Ile Phe Trp Phe His Met Pro Gln Ile Ser Phe
85 90 95
Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His Ser Phe Gln Ala Thr
100 105 110

Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125

Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser Pro Gln Leu Thr Thr
 130 135 140

Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu Ile Thr Thr Phe Pro
 145 150 155 160

Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr Phe Arg Thr Thr Ile
 165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala
 180 185 190

Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu Leu Val Ala Phe Ala
 195 200 205

Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe Ser Tyr Val Arg Ile
 210 215 220

Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala
 225 230 235 240

Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu
 245 250 255

Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ala His Ile Pro
 260 265 270

Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr Leu Leu Val Pro Pro
 275 280 285

Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr Lys Gln Ile Arg Asp
 290 295 300

Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro Leu
 305 310 315

<210> 17

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
 peptide

<400> 17

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10 15

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln
20 25

<210> 18

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 18

Arg Thr Glu His Ser Leu His Glu Pro Met Tyr
1 5 10

<210> 19

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 19

Asn Ser Thr Thr Ile Gln Phe Asp Ala Cys Leu Leu Gln Met
1 5 10

<210> 20

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 20

His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr Lys

1 5 10 15

<210> 21
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 21
Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser Tyr Cys
1 5 10 15

Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg
20 25 30

<210> 22
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 22
Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala
1 5 10

<210> 23
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 23
His Arg Phe Ser Lys Arg Arg Asp Ser Pro
1 5 10

<210> 24
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 24
Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala
1 5 10 15
Thr His Ala Ser Glu Pro
20

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward GPCR9
primer-

<400> 25
cctgtgctca acccaattgt ct 22

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse GPCR9
primer-

<400> 26
actgacacct agggctctga ag 22

<210> 27
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-F3
forward primer

<400> 27

agccgagcca catcgct

17

<210> 28

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-R1
reverse primer

<400> 28

gtgaccaggc gccaatac

19

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-PVIC
Taqman(R) Probe

<400> 29

caaatcgtt gactccgacc ttcacctt

28

<210> 30

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 5'
primer

<400> 30

cccaagcttg caccatgatg gtggatccca atggcattg

39

<210> 31

<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY4 3'
primer

<400> 31
gaagatctct agggctctga agcgtgtgtg gcc 33

<210> 32
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HGPRBMY4 3'
primer- Flag tag

<400> 32
gaagatctct acttgctgctc gtcgtccttg tagtccatgg gctctgaagc gtgtgtggc 59

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 33
Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu
1 5 10

<210> 34
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 34

Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
1 5 10

<210> 35

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 35

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr
1 5 10

<210> 36

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 36

Ala Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu
1 5 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 37

His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu Pro Val Ile
1 5 10

<210> 38

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 38
Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39
Ile Ala Val Leu Gly Asn Leu Thr Ile Ile Tyr Ile Val Arg
1 5 10

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 40
Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp Ala
1 5 10

<210> 41
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 41

Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu
1 5 10 15

<210> 42

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
1 5 10 15

<210> 43

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 43

Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala
1 5 10 15

<210> 44

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 44

Gln Ala Lys Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe
1 5 10 15

<210> 45
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 45
His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe
1 5 10 15

Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
20 25

<210> 46
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide 1

<220>
<221> modified_base
<222> (25)..(84)
<223> n=a+g+c+t; k=c+g+t

<400> 46
cgaagcgtaa gggcccagcc ggccnnknkn nnknknknkn nnknknknkn knknknknkn 60
nnknknknkn nnknknknkn knkccgggt ccgggcggc 99

<210> 47
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide 2 N+A+G+C+T; V=C+A+G

<220>
<221> modified_base

<222> (21)..(80)

<223> n=a+g+c+t; v=c+a+g

<400> 47

aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nnvnnvnnvn gccgcccga cccgg 95

<210> 48

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 48

Pro Gly Pro Gly Gly

1

5

<210> 49

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 49

gcagcagcgg ccgccagttc tggttggcct tcccattg

38

<210> 50

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 50

gcagcagtcg acgggctctg aagcgtgtgt ggccac

36

<210> 51
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 51
gcagcagcgg ccgcatgatg gtggatccca atggcaatg

39

<210> 52
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 52
gcagcagtcg accttcactc catagacaat tgggttg

37

<210> 53
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53
Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp
1 5 10 15

<210> 54
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54

Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
1 5 10 15

<210> 55

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55

Phe Ala Gly Gln Ile Ile Trp Tyr Asp Ala Leu Asp Thr Leu Met
1 5 10 15

<210> 56

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56

Leu Ile Phe Phe Asp Ala Arg Asp Cys Cys Phe Asn Glu Gln Leu
1 5 10 15

<210> 57

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57

Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
1 5 10 15

<210> 58
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 58

Arg Ile Val Pro Asn Gly Tyr Phe Asn Val His Gly Arg Ser Leu
1 5 10 15

<210> 59

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 59

Trp Glu Arg Ser Ser Ala Gly Cys Ala Asp Gln Gln Tyr Arg Cys
1 5 10 15

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 60

Tyr Phe Ser Asp Gly Glu Ser Phe Phe Glu Pro Gly Asp Cys Cys
1 5 10 15